

5' 3' 1' 2' 4' 6' 8' 10' 12' 14' 16' 18' 20' 22' 24' 26' 28' 30' 32' 34' 36' 38' 40' 42' 44' 46' 48' 50' 52' 54' 56' 58' 60' 62' 64' 66' 68' 70' 72' 74' 76' 78' 80' 82' 84' 86' 88' 90' 92' 94' 96' 98' 100'

9	18	27	36	45	54
5' GAC GTG TTT GGC AGC GGG ACG CAC CAT TTC AGT TGT GTT CTT GGT TCA TTT CGT					
63	72	81	90	99	108
GTC TCG GCG ATG TTT CCT AGA GTC TCG ACG TTC CTA CCT CTT CGC CCC CTT TCC					
	M	F	P	R	S
117	126	135	144	153	162
CGC CAC CCT TTG TCC TCT GGA AGC CCG GAG ACA TCA GCG GCT GCG ATT ATG CTA					
R H P L S S G S P E T S A A A I M L					
171	180	189	198	207	216
CTC ACT GTT CGG CAC GGA ACA GTC AGG TAC CGC AGT TCA GCG CTG TTG GCC CGG					
L T V R H G T V R Y R S S A L L A R					
225	234	243	252	261	270
ACA AAA AAT AAC ATC CAA AGA TAT TTT GGC ACT AAC AGT GTG ATC TGT AGC AAG					
T K N N I Q R Y F G T N S V I C S K					
279	288	297	306	315	324
AAA GAT AAG CAG TCT GTT CGA ACT GAG GAG ACT TCC AAG GAG ACT TCA GAG AGC					
K D K Q S V R T E E T S K E T S E S					
333	342	351	360	369	378
CAA GAC AGT GAA AAG GAA AAT ACG AAA AAA GAC TTG TTA GGC ATT ATT AAG GGC					
Q D S E K E N T K K D L L G I I K G					

FIGURE 1A

765	774	783	792	801	810
TAT GAC AAT TAT CCT GGC CAG GAG AAG ACG GAT GAT CTT AAA AGG AAA AAT					
Y D N Y P G Q E K T D D L K K R K N					
819	828	837	846	855	864
ATA TTC ACA GGG AAA AGA CTT AAT ATT TTT GAC ATG ATG GCA GTT ACT AAA GAA					
I F T G K R L N I F D M M A V T K E					
873	882	891	900	909	918
GCA CCT GAA ACA GAC ACA TCA CCT TCA CTT TGG GAT GTG GAA TTT GCT AAG CAG					
A P E T D T S P S L W D V E F A K Q					
927	936	945	954	963	972
TTA GCC ACA GTA AAT GAA CAA CCC CTT CAG AAT GGA TTT GAA GAG CTG ATC CAG					
L A T V N E Q P L Q N G F E L I Q					
981	990	999	1008	1017	1026
TGG ACA AAA GAG GGG AAA CTA TGG GAG TTC CCA ATT AAC AAT GAA GCA GGT TTT					
W T K E G K L W E F P I N N E A G F					
1035	1044	1053	1062	1071	1080
GAT GAT GAT GGT TCA GAA TTT CAT GAA CAT ATA TTT CTG GAG AAA CAC CTG GAG					
D D D G S E F H E H I F L E K H L E					
1089	1098	1107	1116	1125	1134
AGC TTT CCA AAA CAA GGA CCA ATT CGC CAC TTC ATG GAG CTG GTG ACT TGT GGC					
S F P K Q G P I R H F M E L V T C G					

FIGURE 1C

1143	1152	1161	1170	1179	1188
CTT TCC AAA AAC CCA TAT CTT AGT GTT AAA CAG AAG GTT GAA CAC ATA GAG TGG					
L S K N P Y L S V K Q K V E H I E W					
1197	1206	1215	1224	1233	1242
TTT AGA AAT TAT TTT AAT GAA AAA AAG GAT ATT CTA AAA GAA AGT AAC ATA CAG					
F R N Y F N E K K D I L K E S N I Q					
1251	1260	1269	1278	1287	1296
TTC AAT TAA GAC CAT GGA AAT TTT TAT TTC AAA CAA TTA GAG ATG GAT ATT ACA					
F N					
1305	1314				
ACT AAA TAA AAT AAT TGC 3'					

FIGURE 1D

1 MFPRVSTFLPLRPLSRHPLSSGSPETSA AAILLTVRHGT 035842
1 MLHRI PAFLRPRFSGLP LSCGNRDVSV A--VL PAAQSGA GI 1272669

41 VRYRSSALLARTKNNIQRYFGTNSVICSKKDKQSVRTEET 035842
39 VR-----TENNIQRHFCTSR SICSKKVDQSV PAN EI GI 1272669

81 SKETSESQDSEKENTKKDDL LGIIKGMKVELSTVNVRTTKP 035842
70 SQKAAESQGRGKETLKKDDL DIIKDMKV DLS TANVKTPKP GI 1272669

121 PKRRPLKSL EATLGRLRRAT EYAPKKRIEPLSPELVAAAS 035842
110 RGRKPSASLEATVDR LQKAPEDPPKKRNEFLSPELVAAAS GI 1272669

161 AVADSLPF DKQTTKSEL LSQLQQH EESRAQRD AKRPKIS 035842
150 AVADSLPF DKQTTKSEL LSQLQQH EELRAQKD REKRRIS GI 1272669

201 FSNIIISDMKVARSAT ARVRSRP ERLIQFDEGYDNYPGQEK 035842
190 FTHIISNMKI AKSPSGRASTRPQH QIQFDEDM DSS LKQEK GI 1272669

241 TDDLKKRKNIF TGKRLNIFDMM AVTK EAPETDTS PSLWDV 035842
230 PTD FRKRYL FKGKRLSIFADKAFAD EPEPEASPSLW EI GI 1272669

281 EF AKQLATVNEQPLQNGFEEELIQWTK EGK LWEFPINN EAG 035842
270 EF AKQLASVADQPFENGFEEMIQWTK EGK LWEFPVNN EAG GI 1272669

FIGURE 2A

321	F	D	D	D	G	S	E	F	H	E	I	F	L	E	K	H	L	E	S	F	P	K	Q	G	P	I	R	H	F	M	E	L	V	T	C	G	L	S	K	035842
310	L	D	D	D	G	S	E	F	H	E	I	F	L	D	K	Y	L	E	D	F	P	K	Q	G	P	I	R	L	F	M	E	L	V	T	C	G	L	S	K	GI 1272669

361 N P Y L S V K Q K V E H I E W F R N Y F N E K K D I L K E S N I Q F N
250 N P V I S V K Q K V E H I E W F R N Y F N E K R D I L K E N N I A F T

361 NPYLSVKQKVEHIEWFNRNYFNEKKDILKESNIQFN
350 NPYLSVKQKVEHIEWFNRNYFNEKRDILKENNIAFT

FIGURE 2B